

 [ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Swiss-Prot](#) [Proteomics tools](#)

Search for

Sim

Click [here](#) to view these alignments graphically with the [LALNVIEW](#) program (mime-type *chemical/x-aln2*).

Click [here](#) to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a [sample screen](#) of LALNVIEW and access its [documentation](#).

Results of SIM with:

Sequence 1: SEQ (434 residues)

Sequence 2: P10845, (1296 residues)

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 5

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using [PRSS](#) at EMBnet-CH.

99.8% identity in 434 residues overlap; Score: 2296.0; Gap frequency: 0.0%

```
SEQ      1 MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
P10845,  863 LSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
          *****

SEQ      61 KIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGE
P10845,  923 KIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGE
          *****

SEQ      121 IIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPIS
P10845,  983 IIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPIS
          *****

SEQ      181 NLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWG
P10845,  1043 NLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWG
          *****

SEQ      241 DYLYQDKPYMYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFII
P10845,  1103 DYLYQDKPYMYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFII
          *****
```

SEQ 301 KKYASGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
P10845, 1163 KKYASGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVV

SEQ 361 MKSKNDQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRQIERSSRTLGCWS
P10845, 1223 MKSKNDQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRQIERSSRTLGCWS

SEQ 421 EFIPVDDGWGERPL
P10845, 1283 EFIPVDDGWGERPE

34.8% identity in 23 residues overlap; Score: 41.0; Gap frequency: 0.0%

SEQ 207 IKYFNLFDKELNEKEIKDLYDNQ
P10845, 805 VKRLEDFDASLKDALLKYIYDNR
* * * * *

29.4% identity in 34 residues overlap; Score: 39.0; Gap frequency: 0.0%

SEQ 27 IDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
P10845, 367 LNFDAKAVFKINIVPKVNYTIYDGFNLRNTNLAAN
* * * * *


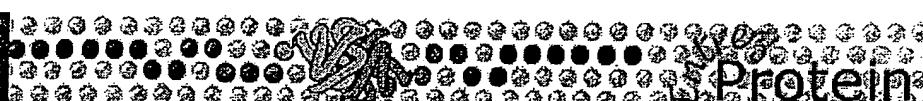
25.0% identity in 28 residues overlap; Score: 39.0; Gap frequency: 0.0%

SEQ 242 YLQYDKPYMYMLNLYDPNKYVDVNNVGIR
P10845, 366 YLNFDKAVFKINIVPKVNYTIYDGFNLR
* * * * *

31.8% identity in 22 residues overlap; Score: 37.0; Gap frequency: 0.0%

SEQ 344 LSALEIPDVGNLSQVVVMKSKN
P10845, 19 IAYIKIPNVGQMOPVKAFKIHN
* * * * *

 [ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Swiss-Prot](#) [Proteomics tools](#)

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

Range: from to
 Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [P10845](#). Reports Botulinum neuroto...[gi:399133] [BLink](#), [Links](#)

LOCUS P10845 1296 aa linear BCT 01-MAY-2005
 DEFINITION Botulinum neurotoxin type A precursor (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain].
 ACCESSION P10845
 VERSION P10845 GI:399133
 DBSOURCE swissprot: locus BXA1_CLOBO, accession [P10845](#); class: standard.
 extra accessions: P01561, P18639, created: Jul 1, 1989.
 sequence updated: Jul 1, 1993.
 annotation updated: May 1, 2005.
 xrefs: [X52066.1](#), [CAA36289.1](#), [M30196.1](#), [AAA23262.1](#), [X92973.1](#), [CAA63551.1](#), [D67030.1](#), [BAA11051.1](#), [M27892.1](#), [AAA23269.1](#), [BTCLAB](#), [3BTAA](#)
 xrefs (non-sequence databases): MEROPSM27.002, InterProIPR008985, InterProIPR011065, InterProIPR006025, InterProIPR000395, PfamPF01742, PRINTSPR00760, ProDomPD001963, PROSITEPS00142
 KEYWORDS 3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Pharmaceutical; Protease; Toxin; Transmembrane; Zinc.
 SOURCE Clostridium botulinum
 ORGANISM [Clostridium botulinum](#)
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
 REFERENCE 1 (residues 1 to 1296)
 AUTHORS Thompson, D.E., Brehm, J.K., Oultram, J.D., Swinfield, T.J., Shone, C.C., Atkinson, T., Melling, J. and Minton, N.P.
 TITLE The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding gene
 JOURNAL Eur. J. Biochem. 189 (1), 73-81 (1990)
 PUBMED [2185020](#)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=Type A / NCTC 2916
 REFERENCE 2 (residues 1 to 1296)
 AUTHORS Binz, T., Kurazono, H., Wille, M., Frevert, J., Wernars, K. and Niemann, H.
 TITLE The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins
 JOURNAL J. Biol. Chem. 265 (16), 9153-9158 (1990)
 PUBMED [2160960](#)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=Type A / 62A
 REFERENCE 3 (residues 1 to 1296)
 AUTHORS East, A.K., Bhandari, M., Stacey, J.M., Campbell, K.D. and Collins, M.D.
 TITLE Organization and phylogenetic interrelationships of genes encoding

components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component

JOURNAL Int. J. Syst. Bacteriol. 46 (4), 1105-1112 (1996)
PUBMED 8863443
REMARK NUCLEOTIDE SEQUENCE OF 1-65.
STRAIN=Type A / 62A

REFERENCE 4 (residues 1 to 1296)
AUTHORS Betley, M.J., Somers, E. and DasGupta, B.R.
TITLE Characterization of botulinum type A neurotoxin gene: delineation of the N-terminal encoding region

JOURNAL Biochem. Biophys. Res. Commun. 162 (3), 1388-1395 (1989)
PUBMED 2669749
REMARK NUCLEOTIDE SEQUENCE OF 1-34.
STRAIN=Type A / Hall

REFERENCE 5 (residues 1 to 1296)
AUTHORS Fujita, R., Fujinaga, Y., Inoue, K., Nakajima, H., Kumon, H. and Oguma, K.
TITLE Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins

JOURNAL FEBS Lett. 376 (1-2), 41-44 (1995)
PUBMED 8521962
REMARK NUCLEOTIDE SEQUENCE OF 1-18.
STRAIN=Type A / NIH

REFERENCE 6 (residues 1 to 1296)
AUTHORS Schmidt, J.J., Sathyamoorthy, V. and DasGupta, B.R.
TITLE Partial amino acid sequence of the heavy and light chains of botulinum neurotoxin type A

JOURNAL Biochem. Biophys. Res. Commun. 119 (3), 900-904 (1984)
PUBMED 6370252
REMARK PROTEIN SEQUENCE OF 1-16.

REFERENCE 7 (residues 1 to 1296)
AUTHORS Dasgupta, B.R., Foley, J. and Niece, R.
TITLE Partial sequence of the light chain of botulinum neurotoxin type A

JOURNAL Biochemistry 26, 4162-4162 (1987)
REMARK PROTEIN SEQUENCE OF 1-46.

REFERENCE 8 (residues 1 to 1296)
AUTHORS DasGupta, B.R. and Dekleva, M.L.
TITLE Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site

JOURNAL Biochimie 72 (9), 661-664 (1990)
PUBMED 2126206
REMARK PROTEIN SEQUENCE OF 1-5 AND 444-456.

REFERENCE 9 (residues 1 to 1296)
AUTHORS Sathyamoorthy, V., Dasgupta, B.R., Foley, J. and Niece, R.L.
TITLE Botulinum neurotoxin type A: cleavage of the heavy chain into two halves and their partial sequences

JOURNAL Arch. Biochem. Biophys. 266 (1), 142-151 (1988)
PUBMED 3178218
REMARK PROTEIN SEQUENCE OF 448-464 AND 872-895.

REFERENCE 10 (residues 1 to 1296)
AUTHORS Shone, C.C., Hambleton, P. and Melling, J.
TITLE Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity

JOURNAL Eur. J. Biochem. 151 (1), 75-82 (1985)
PUBMED 3896784

REMARK PROTEIN SEQUENCE OF 448-482.
REFERENCE 11 (residues 1 to 1296)
AUTHORS Gimenez, J.A. and DasGupta, B.R.
TITLE Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments
JOURNAL J. Protein Chem. 12 (3), 351-363 (1993)
PUBMED [8397793](#)
REMARK PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
REFERENCE 12 (residues 1 to 1296)
AUTHORS Schiavo, G., Santucci, A., Dasgupta, B.R., Mehta, P.P., Jontes, J., Benfenati, F., Wilson, M.C. and Montecucco, C.
TITLE Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds
JOURNAL FEBS Lett. 335 (1), 99-103 (1993)
PUBMED [8243676](#)
REMARK IDENTIFICATION OF SUBSTRATE.
REFERENCE 13 (residues 1 to 1296)
AUTHORS Binz, T., Blasi, J., Yamasaki, S., Baumeister, A., Link, E., Sudhof, T.C., Jahn, R. and Niemann, H.
TITLE Proteolysis of SNAP-25 by types E and A botulinum neurotoxins
JOURNAL J. Biol. Chem. 269 (3), 1617-1620 (1994)
PUBMED [8294407](#)
REMARK IDENTIFICATION OF SUBSTRATE.
REFERENCE 14 (residues 1 to 1296)
AUTHORS Rigoni, M., Caccin, P., Johnson, E.A., Montecucco, C. and Rossetto, O.
TITLE Site-directed mutagenesis identifies active-site residues of the light chain of botulinum neurotoxin type A
JOURNAL Biochem. Biophys. Res. Commun. 288 (5), 1231-1237 (2001)
PUBMED [11700044](#)
REMARK MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
REFERENCE 15 (residues 1 to 1296)
AUTHORS Lacy, D.B., Tepp, W., Cohen, A.C., DasGupta, B.R. and Stevens, R.C.
TITLE Crystal structure of botulinum neurotoxin type A and implications for toxicity
JOURNAL Nat. Struct. Biol. 5 (10), 898-902 (1998)
PUBMED [9783750](#)
REMARK X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
COMMENT On or before Mar 15, 2005 this sequence version replaced [gi:279630](#), [gi:115193](#), [gi:115174](#).
[FUNCTION] Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-I-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure.
[CATALYTIC ACTIVITY] Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
[COFACTOR] Binds 1 zinc ion per subunit.
[SUBUNIT] Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H).
[SUBCELLULAR LOCATION] Secreted.
[PHARMACEUTICAL] Available under the name BOTOX (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial

spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

[MISCELLANEOUS] There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.

[SIMILARITY] Belongs to the peptidase M27 family.

[DATABASE] NAME=BOTOX product information Web site;

WWW='<http://www.botox.com/site/>'.

[DATABASE] NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;

WWW='http://www.expasy.org/spotlight/back_issues/sptlt019.shtml'.

FEATURES	Location/Qualifiers
source	1..1296 /organism="Clostridium botulinum" /db_xref="taxon:1491"
gene	1..1296 /gene="botA" /note="synonyms: atx, bna"
<u>Protein</u>	1..1296 /gene="botA" /product="Botulinum neurotoxin type A precursor" /EC_number="3.4.24.69"
<u>Region</u>	2..448 /gene="botA" /region_name="Mature chain" /note="Botulinum neurotoxin A light-chain." /evidence=experimental
<u>Region</u>	2 /gene="botA" /region_name="Conflict" /note="P -> Q (in Ref. 1)." /evidence=experimental
<u>Region</u>	10..11 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	19..23 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	26 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	27 /gene="botA" /region_name="Variant" /note="V -> A." /evidence=experimental
<u>Region</u>	33..39 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	40..41 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	42..48 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	54..56

	/gene="botA"
	/region_name="Helical region"
<u>Region</u>	/evidence=experimental
	75..78
	/gene="botA"
	/region_name="Hydrogen bonded turn"
<u>Region</u>	/evidence=experimental
	81..99
	/gene="botA"
<u>Region</u>	/region_name="Helical region"
	/evidence=experimental
	100
	/gene="botA"
	/region_name="Hydrogen bonded turn"
<u>Region</u>	/evidence=experimental
	102..113
	/gene="botA"
	/region_name="Helical region"
<u>Region</u>	/evidence=experimental
	120..121
	/gene="botA"
	/region_name="Hydrogen bonded turn"
<u>Region</u>	/evidence=experimental
	124..125
	/gene="botA"
	/region_name="Hydrogen bonded turn"
<u>Region</u>	/evidence=experimental
	131..133
	/gene="botA"
	/region_name="Helical region"
<u>Region</u>	/evidence=experimental
	134..138
	/gene="botA"
	/region_name="Beta-strand region"
<u>Region</u>	/evidence=experimental
	140..141
	/gene="botA"
	/region_name="Hydrogen bonded turn"
<u>Region</u>	/evidence=experimental
	144..148
	/gene="botA"
	/region_name="Beta-strand region"
<u>Region</u>	/evidence=experimental
	151..155
	/gene="botA"
	/region_name="Beta-strand region"
<u>Region</u>	/evidence=experimental
	160..161
	/gene="botA"
	/region_name="Hydrogen bonded turn"
<u>Region</u>	/evidence=experimental
	164..166
	/gene="botA"
	/region_name="Beta-strand region"
<u>Region</u>	/evidence=experimental
	168
	/gene="botA"
	/region_name="Beta-strand region"
<u>Region</u>	/evidence=experimental
	175..177

```

/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 184..187
/region_name="Beta-strand region"
/evidence=experimental
Region 192..193
/region_name="Beta-strand region"
/evidence=experimental
Region 195..196
/region_name="Beta-strand region"
/evidence=experimental
Region 201..203
/region_name="Helical region"
/evidence=experimental
Region 204
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 206..207
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 213..214
/region_name="Beta-strand region"
/evidence=experimental
Region 217..232
/region_name="Helical region"
/evidence=experimental
Site 223
/site_type="metal-binding"
/note="Zinc (catalytic)."
```

Site 224

```

/site_type="active"
/evidence=experimental
Site 227
/site_type="metal-binding"
/note="Zinc (catalytic)."
```

Region 233..234

```

/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 239..240
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 242
/region_name="Beta-strand region"
```



```

      /evidence=experimental
Region      245
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region      252
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region      259
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region      260..266
      /gene="botA"
      /region_name="Helical region"
      /evidence=experimental
Site       262
      /gene="botA"
      /site_type="metal-binding"
      /note="Zinc (catalytic)."
```

Site 262

```

      /evidence=experimental
      /gene="botA"
      /site_type="mutagenized"
      /note="E->A: Drastic decrease in enzymatic activity."
      /evidence=experimental
Site       266
      /gene="botA"
      /site_type="mutagenized"
      /note="F->A: Decreases enzymatic activity."
      /evidence=experimental
Region      268..269
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region      270..273
      /gene="botA"
      /region_name="Helical region"
      /evidence=experimental
Region      276..298
      /gene="botA"
      /region_name="Helical region"
      /evidence=experimental
Region      299
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region      306
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region      310..321
      /gene="botA"
      /region_name="Helical region"
      /evidence=experimental
Region      322
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental

```

Region 324..325
 /gene="botA"
 /region_name="Beta-strand region"
 /evidence=experimental

Region 331..332
 /gene="botA"
 /region_name="Beta-strand region"
 /evidence=experimental

Region 335..347
 /gene="botA"
 /region_name="Helical region"
 /evidence=experimental

Region 348
 /gene="botA"
 /region_name="Hydrogen bonded turn"
 /evidence=experimental

Region 351..357
 /gene="botA"
 /region_name="Helical region"
 /evidence=experimental

Region 358..359
 /gene="botA"
 /region_name="Hydrogen bonded turn"
 /evidence=experimental

Region 366..367
 /gene="botA"
 /region_name="Hydrogen bonded turn"
 /evidence=experimental

Site 366
 /gene="botA"
 /site_type="mutagenized"
 /note="Y->A: Decreases enzymatic activity."
 /evidence=experimental

Region 374..375
 /gene="botA"
 /region_name="Beta-strand region"
 /evidence=experimental

Region 381..383
 /gene="botA"
 /region_name="Hydrogen bonded turn"
 /evidence=experimental

Region 385
 /gene="botA"
 /region_name="Beta-strand region"
 /evidence=experimental

Region 386..388
 /gene="botA"
 /region_name="Hydrogen bonded turn"
 /evidence=experimental

Region 389
 /gene="botA"
 /region_name="Beta-strand region"
 /evidence=experimental

Region 390
 /gene="botA"
 /region_name="Hydrogen bonded turn"
 /evidence=experimental

Region 402..404
 /gene="botA"
 /region_name="Helical region"

```

Region      /evidence=experimental
            405
            /gene="botA"
            /region_name="Beta-strand region"
            /evidence=experimental
Region      406..409
            /gene="botA"
            /region_name="Hydrogen bonded turn"
            /evidence=experimental
Region      410..412
            /gene="botA"
            /region_name="Helical region"
            /evidence=experimental
Region      414..415
            /gene="botA"
            /region_name="Beta-strand region"
            /evidence=experimental
Region      421..423
            /gene="botA"
            /region_name="Hydrogen bonded turn"
            /evidence=experimental
Region      426..431
            /gene="botA"
            /region_name="Beta-strand region"
            /evidence=experimental
Bond        bond(430,454)
            /gene="botA"
            /bond_type="disulfide"
            /note="Interchain (between light and heavy chains)."
```

Region 449..1296

```

            /gene="botA"
            /region_name="Mature chain"
            /note="Botulinum neurotoxin A heavy-chain."
            /evidence=experimental
Region      454..458
            /gene="botA"
            /region_name="Beta-strand region"
            /evidence=experimental
Region      459..461
            /gene="botA"
            /region_name="Helical region"
            /evidence=experimental
Region      463
            /gene="botA"
            /region_name="Beta-strand region"
            /evidence=experimental
Region      466
            /gene="botA"
            /region_name="Beta-strand region"
            /evidence=experimental
Region      468..470
            /gene="botA"
            /region_name="Hydrogen bonded turn"
            /evidence=experimental
Region      475..476
            /gene="botA"
            /region_name="Hydrogen bonded turn"
            /evidence=experimental
Region      479..481
```

	/gene="botA"
	/region_name="Beta-strand region"
	/evidence=experimental
<u>Region</u>	480
	/gene="botA"
	/region_name="Conflict"
	/note="E -> P (in Ref. 9)."
	/evidence=experimental
<u>Region</u>	496..504
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	505
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	517
	/gene="botA"
	/region_name="Beta-strand region"
	/evidence=experimental
<u>Region</u>	525
	/gene="botA"
	/region_name="Beta-strand region"
	/evidence=experimental
<u>Region</u>	528
	/gene="botA"
	/region_name="Beta-strand region"
	/evidence=experimental
<u>Region</u>	542..545
	/gene="botA"
	/region_name="Beta-strand region"
	/evidence=experimental
<u>Region</u>	550..555
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	556..557
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	573..576
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	577
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	579..580
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	588..594
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	600..601
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental

```

Region      604..617
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      618..619
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      622
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      625..626
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      627..647
               /gene="botA"
               /region_name="Transmembrane region"
               /note="Potential."
               /evidence=not_experimental
Region      628..629
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      633
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      635..637
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      638..644
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      652..659
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      656..676
               /gene="botA"
               /region_name="Transmembrane region"
               /note="Potential."
               /evidence=not_experimental
Region      661..664
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      679..681
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      685..686
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      688..720
               /gene="botA"

```

	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	721
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	722..742
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	743..745
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	746..751
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	752..753
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	758..759
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	766..799
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	800
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	801..824
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	825..829
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	831..833
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	834..835
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	836..844
	/gene="botA"
	/region_name="Helical region"
	/evidence=experimental
<u>Region</u>	845..846
	/gene="botA"
	/region_name="Hydrogen bonded turn"
	/evidence=experimental
<u>Region</u>	853..855
	/gene="botA"

```

      /region_name="Helical region"
      /evidence=experimental
Region 860..871
      /gene="botA"
      /region_name="Helical region"
      /evidence=experimental
Region 873..876
      /gene="botA"
      /region_name="Helical region"
      /evidence=experimental
Region 876
      /gene="botA"
      /region_name="Conflict"
      /note="T -> L (in Ref. 8)."
```

```

      /evidence=experimental
Region 879..884
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region 885..886
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region 887..890
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region 891..892
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region 892
      /gene="botA"
      /region_name="Conflict"
      /note="S -> K (in Ref. 8)."
```

```

      /evidence=experimental
Region 895..900
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region 905..906
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region 911..912
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region 913..917
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
Region 920..921
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region 924..928
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
```

<u>Region</u>	931..932 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	935..938 /gene="botA" /region_name="Helical region" /evidence=experimental
<u>Region</u>	941..948 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	956..959 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	961..966 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	975..979 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	982..988 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	990..991 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	994..1000 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1011..1012 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1014..1021 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1023..1024 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1026..1031 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1032..1033 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1034..1040 /gene="botA" /region_name="Beta-strand region" /evidence=experimental

<u>Region</u>	1042..1043 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1052..1058 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1063..1064 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1066..1075 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1081..1090 /gene="botA" /region_name="Helical region" /evidence=experimental
<u>Region</u>	1091..1092 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1094..1095 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1096 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1098 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1100..1101 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1104 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1106 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1111..1113 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1119..1120 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1122..1125 /gene="botA" /region_name="Beta-strand region" /evidence=experimental

<u>Region</u>	1130..1131 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1134..1137 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1142 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1152 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1159..1163 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1173 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1175 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1176..1177 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1179..1186 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1187..1188 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1189..1195 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1197..1198 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1207..1209 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1211..1213 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1215..1216 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental

```

Region      1218
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1218
               /gene="botA"
               /region_name="Conflict"
               /note="S -> Y (in Ref. 11)."
               /evidence=experimental
Region      1221..1223
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1226
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1228..1229
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1232
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Bond        bond(1235,1280)
               /gene="botA"
               /bond_type="disulfide"
               /evidence=experimental
Region      1235
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1237..1239
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1242..1243
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1248..1253
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1260..1264
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1265..1270
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      1271..1272
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1279..1280
               /gene="botA"
               /region_name="Hydrogen bonded turn"

```

Region /evidence=experimental
1281
/gene="botA"
/region_name="Beta-strand region"
/evidence=experimental
Region 1284..1285
/gene="botA"
/region_name="Beta-strand region"
/evidence=experimental
Region 1289..1290
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental

ORIGIN

```
1 mpfvnkqfny kdpvngvdia yikipnvqgm qpvkafkihn kiwviperdt ftnpeegdlm
61 pppeakqvqv sydstylst dnekdnylkg vtlkferiys tdlgrmltts ivrgipfwgg
121 stidtelkvi dtncinviqp dgsyrseeln lviigpsadi iqfecksfgh evlnltrngy
181 gstqyirfsp dftfgfeesl evdtnpllg gkfatdpavt laheliagh rlygiainp
241 rvfkvnntay yemsglevsf eelrtfgghd akfidslqen efrlyyyknf kdiastlnka
301 ksivgttasl qymknvfkek yllsedtsqk fsvdklkfdk lykmlteiyt ednfvkffkv
361 lnrktylnfd kavfkinivp kvnytiydgf nlrntnlaan fngqnteinn mnftklknft
421 glfefykllc vrgiitsktk sldkgynkal ndlcikvnnw dlffspsedn ftndlnkgee
481 itsdtnieaa eenisldliq qyyltfnfdn epenisienl ssdiigglel mpnierfpng
541 kkyeldkytm fhylraqefe hgksrialtn svneallnps rvytffssdy vkkvnkatea
601 amflgwveql vydfdetse vsttdkiadi tiiipyigpa lnignmlykd dfvgalifsg
661 avillefipe iaipvlgtfa lvsyiankv tvqtidnals krnekwdevy kyivtnwlak
721 vntqidlirk kmkealenqa eatkaiinyq ynqyteeeen ninfniddls sklneinka
781 mininkflnq csvsylvmsm ipygvkrled fdaslkdall kyidnrgtl igqvdrldk
841 vnntlstdip fqlskyvndq rllstfteyi kniintsiln lryesnhlid lsryaskini
901 gskvnfdpid knqiqlfnle sskievilk aivynsmyen fstsfwirip kyfnsisl
961 eytiincmen nsgwkvslny geiiwtlqdt qeikqrvvfk ysqminisdy inrwifvtit
1021 nnrlnnskiy ingrlidqkp isnlgnihas nnimfkldgc rdthryiwik yfnlfdkeln
1081 ekeikdlydn qsnsgilkdf wgdylqydkp yymlnlydpn kyvdvnnvqi rgymylkgpr
1141 gsvmttniyl nsslyrgtkf iikkyasgnk dnivrndrv yinvvvknke yrlatnasqa
1201 gvekilsale ipdvgnlsqv vvmkskndqg itnkckmnlq dnngndigfi gfhqfnniak
1261 lvasnwynrq ierssrtlgc swefipvddg wgerpl
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

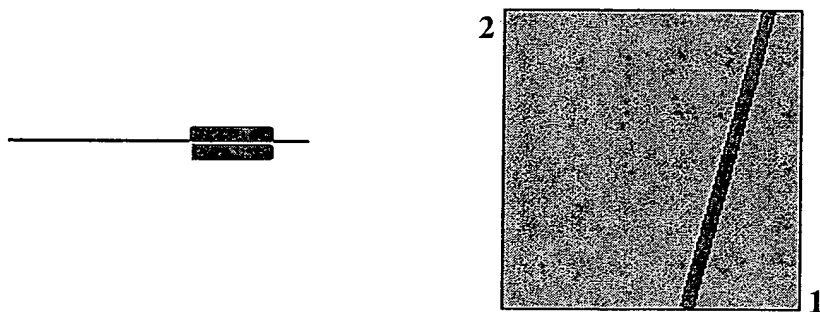
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 1 [gi_144864](#) C.botulinum neurotoxin gene, complete cds. **Length** 4835 (1 .. 4835)

Sequence 2 lcl|seq 2

Length 1323 (1 .. 1323)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 412 bits (214), Expect = e-111

Identities = 937/1302 (71%)

Strand = Plus / Plus

Query: 2947 tctacatttactgaatatattaagaatattattaatacttctatattgaatttaagatat 3006
 ||||| || ||||| || ||||| || || ||||| || || ||||| | ||
 Sbjct: 16 tctaccttactgaatacatcaagaacatcatcaatacctccatcctgaacctgcgctac 75

Query: 3007 gaaagtaatcatttaatagacttatctagggtatgcataaaaaataaatattggtagtaaa 3066
||| |||| | || ||| | || | || |||| || || ||
Sbjct: 76 gaatccaatcacctgatcgacctgtctcgctacgcttccaaaatcaacatcggttctaaa 135

Query: 3067 gtaaattttgatccaatagataaaaaatcaaattcaattattttaatttagaaagtagtaaa 3126
 || || || |||| || || || |||| || || | || || | || |
 Sbjct: 136 gttaacttcgatccgatcgacaagaatcagatccagctgttcaatctggaatcttccaaa 195

Query: 3127 attgaggtaatTTTAAAAAatgctattgtatataatagtatgtatgaaaatttttagtact 3186
 || || || || | || ||||| |||| || ||||| ||||| || ||
 Sbjct: 196 atcgaagttatcctgaagaatgctatcgtatacaactctatgtacgaaaacttctccacc 255

h cb h g b b e b cg

X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)


```

LOCUS       CLONEUR                      4835 bp    DNA        linear        BCT 26-APR-1993
DEFINITION  C.botulinum neurotoxin gene, complete cds.
ACCESSION   M30196
VERSION     M30196.1   GI:144864
KEYWORDS    neurotoxin.
SOURCE      Clostridium botulinum
  ORGANISM  Clostridium botulinum
            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
            Clostridium.
REFERENCE   1 (bases 1 to 4835)
AUTHORS     Binz,T., Kurazono,H., Wille,M., Frevert,J., Wernars,K. and
            Niemann,H.
TITLE       The complete sequence of botulinum neurotoxin type A and comparison
            with other clostridial neurotoxins
JOURNAL     J. Biol. Chem. 265 (16), 9153-9158 (1990)
PUBMED      2160960
COMMENT     Original source text: C.botulinum (strain 62A, subtype A) DNA.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by H.Niemann, 29-NOV-1989.

FEATURES             Location/Qualifiers
     source            1..4835
                     /organism="Clostridium botulinum"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:1491"
     mRNA            240..>4835
                     /product="neurotoxin mRNA"
     misc signal    344..349
                     /note="ribosome binding site"
     CDS             358..4248
                     /note="neurotoxin"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="AAA23262.1"
                     /db_xref="GI:144865"
                     /translation="MPFVNKQFNYKDPVNGVDIAYIKIPNAGQMOPVKAFKIHNKIWW
IPERDFTFTNP EEGDLNPPPEAKQVPVSYDDSTYLSTDNEKDNYLKGVTKLFERIYSTD
LGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSRSEELNLVIIGPSADI
IQFECKSFGHEVLNLTNRNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGA GKFATDPA
VTLAHELIIHAGHRLYGI AINPNRVFKVNTNAYEYMSGLEVNFKEKYLLSEDTSGKFSVD
LQENEFRLYYYNKF KDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVD
KLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNL
RNTNLAANFNGQNT EINNMFNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKAL
NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNF
DNEPENISIENLSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAOEF EHGKSRI

```

ALTNSVNEALLNPSRVYTFSSDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTT
 DKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALV
 SYIANKVLTQVIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQA
 EATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMN
 SMIPYGVKRLEDFDASLKDALLKYIYDNRGTLIGQVDRDKDKVNNTLSTDIPFQLSKY
 VDNQRLSTFTEYIKNIINTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQI
 QLFNLESSKIEVILKNAIVYNSMYENFSTFSWIRIPKYFNSISLNNEYTIINCMMENS
 GWKVSILNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIY
 INGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIWIKYFNLFDKELNEKEIKDLY
 DNQSNSSGILKDFWGDYLDKPYMNLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTT
 NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEK
 ILSALEIPDVGNLQVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNAKLK
 ASNWYNRQIERSSRTLGCSEFIPVDDGWGERPL"

misc feature

4400..4432

/note="potential terminator; putative"

ORIGIN

```

1  aagcttctaa atttaaatta ttaagtataa atccaaataa acaatatgtt caaaaacttg
61 atgaggtaat aatttctgta ttagataata tggaaaaata tatagatata tctgaagata
121 atagattgca actaatagat aacaaaaata acgcaaagaa gatgataatt agtaatgata
181 tatttatttc caattgttta accctatctt ataacggtaa atatatatgt ttatctatga
241 aagatgaaaa ccataattgg atgatatgta ataatgatat gtcaaagtat ttgtatttat
301 ggtcatttaa ataattaata atttaattaa ttttaaatat tataagaggt gttaaatatg
361 ccatttgtaa ataaacaatt taattataaa gatcctgtaa atggtgttga tattgcttat
421 ataaaaattc caaatgcagg acaaatgcaa ccagtaaaag cttttaaaat tcataataaa
481 atatgggtta ttccagaaaag agatacattt acaaatcctg aagaaggaga tttaaatcca
541 ccaccagaag caaaacaagt tccagtttca tattatgatt caacatatatt aagtacagat
601 aatgaaaaag ataattattt aaagggaggt acaaaattat ttgagagaat ttattcaact
661 gatcttggaa gaatgttggt aacatcaata gtaaggggaa taccattttg ggggtggaagt
721 acaatagata cagaattaaa agttattgat actaattgta ttaatgtgat acaaccagat
781 ggtagttata gatcagaaga acttaattct gtaataatag gaccctcagc tgatattata
841 cagtttgaat gtaaaagcgt tggacatgaa gttttgaatc ttacgcgaaa tggttatggc
901 tctactcaat acattagatt tagcccagat tttacatttg gttttgagga gtcacttgaa
961 gttgatacaa atcctctttt aggtgcaggc aaatttgcta cagatccagc agtaacatta
1021 gcacatgaac ttatacatgc tggacataga ttatatggaa tagcaattaa tccaaatagg
1081 gtttttaaaag taaatactaa tgcctattat gaaatgagtg ggtagaagt aagctttgag
1141 gaacttagaa catttggggg acatgatgca aagtttatag atagtttaca ggaaaacgaa
1201 tttcgtctat attattataa taagtttaaa gatatagcaa gtacacttaa taaagctaaa
1261 tcaatagtag gtactactgc ttcattacag tatatgaaaa atgtttttaa agagaaatat
1321 ctctatctg aagatacatc tggaaaattt tcggtagata aattaaaatt tgataagtta
1381 tacaaaatgt taacagagat ttacacagag gataattttg ttaagttttt taaagtactt
1441 aacagaaaaa catatttgaa ttttgataaa gccgtattta agataaatat agtacctaag
1501 gtaaattaca caatatatga tggatttaat ttaagaaata caaatttagc agcaaacttt
1561 aatggtcaaa atacagaaat taataatatg aattttacta aactaaaaaa ttttactgga
1621 ttgtttgaat tttataagtt gctatgtgta agagggataa taacttctaa aactaaatca
1681 ttagataaaag gatacaataa ggcattaaat gatttatgta tcaaagttaa taattgggac
1741 ttgtttttta gtccttcaga agataatttt actaatgac taaataaagg agaagaaatt
1801 acatctgata ctaatataga agcagcagaa gaaaatatta gtttagattt aatacaacaa
1861 tattatttaa cctttaattt tgataatgaa cctgaaaata tttcaataga aaatctttca
1921 agtgacatta taggccaatt agaacttatg cctaatatag aaagatttcc taatggaaaa
1981 aagtatgagt tagataaata tactatgttc cattatcttc gtgctcaaga atttgaacat
2041 ggtaaatcta ggattgcttt aacaaattct gttaacgaag cattattaaa tcctagtcgt
2101 gtttatacat ttttttcttc agactatgta aagaaagtta ataaagctac ggaggcagct
2161 atgtttttag gctgggtaga acaattagta tatgatttta ccgatgaaac tagcgaagta
2221 agtactacgg ataaaattgc ggatataact ataattattc catatatagg acctgcttta
2281 aatataggta atatgttata taaagatgat tttgtaggtg ctttaatat ttcaggagct
2341 gttattctgt tagaatttat accagagatt gcaatacctg tattaggtac ttttgcactt
2401 gtatcatata ttgcgaataa ggttctaacc gttcaaacia tagataatgc ttttaagtaa
2461 agaaatgaaa aatgggatga ggtctataaa tatatagtaa caaattgggt agcaaagggt
2521 aatacacaga ttgatctaata agaaaaaaa atgaaagaag ctttagaaaa tcaagcagaa
2581 gcaacaaagg ctataataaa ctatcagtat aatcaatata ctgaggaaga gaaaaataat

```

2641 attaatttta atattgatga ttttaagttcg aaacttaatg agtctataaa taaagctatg
2701 attaataata ataaattttt gaatcaatgc tctgtttcat atttaatgaa ttctatgatc
2761 ccttatgggtg ttaaacgggt agaagatttt gatgctagtc ttaaagatgc attattaaag
2821 tatatatatg ataatagagg aactttaatt ggtcaagtag atagattaaa agataaagtt
2881 aataatacac ttagtacaga tatacctttt cagctttcca aatacgtaga taatcaaaga
2941 ttattatcta catttactga atatattaag aatattatta atacttctat attgaattta
3001 agatatgaaa gtaatcattt aatagactta tctaggtag catcaaaaat aaatattggt
3061 agtaaagtaa attttgatcc aatagataaa aatcaaattc aattatttaa tttagaaggt
3121 agtaaaattg aggtaatttt aaaaaatgct attgtatata atagtatgta tgaaaatttt
3181 agtactagct tttggataag aattcctaag tattttaaca gtataagtct aaataatgaa
3241 tatacaataa taaattgtat ggaaaataat tcaggatgga aagtatcact taattatggt
3301 gaaataatct ggactttaca ggatactcag gaaataaaac aaagagtagt ttttaatac
3361 agtcaaatga ttaatatatc agattatata aacagatgga tttttgtaac tatcactaat
3421 aatagattaa ataactctaa aatttatata aatggaagat taatagatca aaaaccaatt
3481 tcaaatttag gtaatattca tgctagtaat aatataatgt ttaaattaga tgggtgtaga
3541 gatacacata gatataattg gataaaatat tttaatcttt ttgataagga attaaatgaa
3601 aaagaaatca aagatttata tgataatcaa tcaaattcag gtattttaaa agacttttgg
3661 ggtgattatt tacaatatga taaaccatac tatatgttaa atttatatga tccaaataaa
3721 tatgtcgatg taaataatgt aggtattaga ggttatatgt atcttaaagg gcctagaggt
3781 agcgtaatga ctacaaacat ttattttaa ataaagttgt atagggggac aaaatttatt
3841 ataaaaaaat atgcttctgg aaataaagat aatattgtta gaaataatga tcgtgtatat
3901 attaatgtag tagttaaaaa taaagaatat aggttagcta ctaatgcac acaggcaggc
3961 gtagaaaaaa tactaagtgc attagaaata cctgatgtag gaaatctaag tcaagtagta
4021 gtaatgaagt caaaaaatga tcaaggaata acaaaataaat gcaaaatgaa ttacaagat
4081 aataatggga atgatatagg ctttatagga tttcatcagt ttaataatat agctaaacta
4141 gtagcaagta attggtataa tagacaaata gaaagatcta gtaggacttt gggttgctca
4201 tgggaattta ttctgtaga tgatggatgg ggagaaaggc cactgtaatt aatctcaaac
4261 tacatgagtc tgtcaagaat ttctgtaaa catccataaa aattttaaaa ttaatatggt
4321 taagaataac tagatatgag tattgtttga actgcccctg tcaagtagac aggtaaaaaa
4381 ataaaaatta agatactatg gtctgatttc gatattctat cggagtcaga ctttttaact
4441 tttcttgtat cttttttgta ttgtaaaact ctatgtattc atcaattgca agttccaatt
4501 agtcaaaatt atgaaacttt ctaagataat acatttctga ttttataatt tcccaaaatc
4561 cttccatagg accattatca atacatctac caactcgaga catactttga gttgcgccta
4621 tctcattaag tttattcttg aaagatttac ttgtatattg aaaaccgcta tcaactgtgaa
4681 aaagtggact agcatcagga ttggaggtaa ctgctttatc aaaggtttca aagacaagga
4741 cgttgttatt tgattttcca agtacatagg aaataatgct attatcatgc aaatcaagta
4801 tttcactcaa gtacgccttt gtttcgtctg ttaac

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

Range: from to ☐ Reverse complemented strand Features: ☐ SNP

☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [M30196](#). Reports *C.botulinum* neuro...[gi:144864] [Links](#)

LOCUS CLONEUR 4835 bp DNA linear BCT 26-APR-1993
DEFINITION *C.botulinum* neurotoxin gene, complete cds.
ACCESSION M30196
VERSION M30196.1 GI:144864
KEYWORDS neurotoxin.
SOURCE *Clostridium botulinum*
ORGANISM *Clostridium botulinum*
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
REFERENCE 1 (bases 1 to 4835)
AUTHORS Binz,T., Kurazono,H., Wille,M., Frevert,J., Wernars,K. and
Niemann,H.
TITLE The complete sequence of botulinum neurotoxin type A and comparison
with other clostridial neurotoxins
JOURNAL J. Biol. Chem. 265 (16), 9153-9158 (1990)
PUBMED 2160960
COMMENT Original source text: *C.botulinum* (strain 62A, subtype A) DNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by H.Niemann, 29-NOV-1989.
FEATURES
source Location/Qualifiers
1..4835
/organism="Clostridium botulinum"
/mol_type="genomic DNA"
/db_xref="taxon:1491"
mRNA 240..>4835
/product="neurotoxin mRNA"
misc_signal 344..349
/note="ribosome binding site"
CDS 358..4248
/note="neurotoxin"
/codon_start=1
/transl_table=11
/protein_id="AAA23262.1"
/db_xref="GI:144865"
/translation="MPFVNKQFNYKDPVNGVDIAYIKIPNAGQMOPVKAFKIHNKIWW
IPERDTFTNP EEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNYLKGVTKLFERIYSTD
LGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELNLVIGPSADI
IQFECKSFGHEVLNLTRNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAQKFDPA
VTLAHELHAGHRLYGIAINPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDS
LQENEFRLYYYNKFKDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVD
KLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDAVFKINIVPKVNYTIYDGFNL
RNTNLAANFNGQNT EINNMF TKLNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKAL
NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITS DTNIEAAEENISLDLIQQYYLTFNF
DNEPENISIENLSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEGHKSRI

ALTNSVNEALLNPSRVYTFSSDYVKVKNKATEAAMFLGWVEQLVYDFTDETSEVSTT
 DKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALV
 SYIANKVLTVQIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLRKKMKEALENQA
 EATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMN
 SMIPYGVKRLDFDASLKDALIKYIDNRGTLIGQVDRLKDKVNNTLSTDIPFQLSKY
 VDNQRLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQI
 QLFNLESSKIEVILKNAIVYNSMYENFSTFSWIRIPKYFNSISLNNEYTIINCMENNS
 GWKVS LNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIY
 INGRLLDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLY
 DNQSN SGILKDFWGDYLDQYDKPYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTT
 NIYLNSSLYRGTKFIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEK
 ILSALEIPDVG NLSQVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFN NIAKLV
 ASNWYNRQIERSSRTLGSWEFIPVDDGWGERPL"

misc feature

4400..4432

/note="potential terminator; putative"

ORIGIN

```

1 aagcttctaa atttaaatta ttaagtataa atccaaataa acaatatgtt caaaaacttg
61 atgaggtaat aatttctgta ttagataata tggaaaaata tatagatata tctgaagata
121 atagattgca actaatagat aacaaaaata acgcaaagaa gatgataatt agtaatgata
181 tatttatttc caattgttta accctatctt ataacggtaa atatatatgt ttatctatga
241 aagatgaaaa ccataattgg atgatatgta ataattgatat gtcaaagtat ttgtatttat
301 ggctatttaa ataattaata atttaattaa ttttaaatat tataagaggt gttaaatatg
361 ccatttggtta ataaacaatt taattataaa gatcctgtaa atgggtgttg tattgcttat
421 ataaaaattc caaatgcagg acaaatgcaa ccagtaaaag cttttaaaat tcataataaa
481 atatgggtta ttccagaaaag agatacattt acaaatcctg aagaaggaga tttaaatcca
541 ccaccagaag caaaacaagt tccagtttca tattatgatt caacatattt aagtacagat
601 aatgaaaaag ataattattt aaagggaggt acaaaattat ttgagagaat ttattcaact
661 gatcttgtaa gaatgttggt aacatcaata gtaaggggaa taccattttg ggggtggaagt
721 acaatagata cagaattaaa agttattgat actaattgta ttaatgtgat acaaccagat
781 ggtagtata gatcagaaga acttaattcta gtaataatag gaccctcagc tgatattata
841 cagtttgaat gtaaaagctt tggacatgaa gttttgaate ttacgcgaaa tgggtatggc
901 tctactcaat acattagatt tagccagat ttacatttg gttttgagga gtcacttgaa
961 gttgatacaa atcctctttt aggtgcaggc aaatttgcta cagatccagc agtaacatta
1021 gcacatgaac ttatacatgc tggacataga ttatatggaa tagcaattaa tccaaatagg
1081 gtttttaaa taaatactaa tgcctattat gaaatgagtg ggtagaagt aagctttgag
1141 gaacttagaa catttggggg acatgatgca aagtttatag atagtttaca ggaaaacgaa
1201 tttcgtctat attattataa taagtttaaa gatatagcaa gtacacttaa taaagctaaa
1261 tcaatagtag gtactactgc ttcattacag tatatgaaaa atgtttttta agagaaatat
1321 ctctatctg aagatacatc tggaaaattt tcggtagata aattaaaatt tgataagtta
1381 tacaaaatgt taacagagat ttacacagag gataattttg ttaagtttt taaagtactt
1441 aacagaaaaa catatttgaa ttttgataaa gccgtattta agataaatat agtacctaag
1501 gtaaattaca caatatatga tggatttaat ttaagaaata caaatttagc agcaaacttt
1561 aatggtcaaa atacagaaat taataatatg aattttacta aactaaaaaa ttttactgga
1621 ttgtttgaat tttataagtt gctatgtgta agagggataa taacttctaa aactaaatca
1681 ttagataaaag gatacaataa ggcatttaat gatttatgta tcaaagttta taattgggac
1741 ttgtttttta gtccttcaga agataatttt actaatgac taaataaagg agaagaaatt
1801 acatctgata ctaatataga agcagcagaa gaaaatatta gtttagattt aatacaacaa
1861 tattatttaa cctttaattt tgataatgaa cctgaaaata tttcaataga aaatctttca
1921 agtgacatta taggccaatt agaacttatg cctaatatag aaagatttcc taatggaaaa
1981 aagtatgagt tagataaata tactatgttc cattatcttc gtgctcaaga atttgaacat
2041 ggtaaatcta ggattgcttt aacaaattct gttaacgaag cattattaaa tcctagtcgt
2101 gtttatacat tttttcttc agactatgta aagaaagtta ataaagctac ggaggcagct
2161 atgtttttag gctgggtaga acaattagta tatgatttta ccgatgaaac tagcgaagta
2221 agtactacgg ataaaattgc ggatataact ataattattc catatatagg acctgcttta
2281 aatataggtta atatgttata taaagatgat tttgtaggtg ctttaatat ttcaggagct
2341 gttattctgt tagaatttat accagagatt gcaatacctg tattaggtac ttttgcactt
2401 gtatcatata ttgcgaataa ggttctaacc gttcaaacia tagataatgc ttttaagtaa
2461 agaaatgaaa aatgggatga ggtctataaa tatatagtaa caaattgggt agcaaagggt
2521 aatacacaga ttgatctaata agaaaaaaa atgaaagaag ctttagaaaa tcaagcagaa
2581 gcaacaaagg ctataataaa ctatcagtat aatcaatata ctgaggaaga gaaaaataat


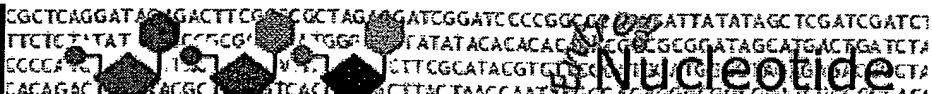
```

2641 attaatTTTta atattgatga tTTaagttcg aaacttaatg agtctataaa taaagctatg
2701 attaatataa ataaatTTTT gaatcaatgc tctgtttcat atttaatgaa ttctatgatc
2761 ccttatggTg tTaaacggTt agaagatTTT gatgctagtc tTaaagatgc attattaaag
2821 tatatatatg ataatagagg aactTTtaatt ggtcaagtag atagattaaa agataaagTt
2881 aataatacac ttagtacaga tatacctTTT cagctTTcca aatacgtaga taatcaaaga
2941 ttattatcta catttactga atatatTaa aatattatta atacttctat attgaattta
3001 agatatgaaa gtaatcattt aatagactta tctaggtag catcaaaaat aaatattggt
3061 agtaaagtaa atTTtgatcc aatagataaa aatcaaattc aattattTaa tttagaaagt
3121 agtaaaattg aggtaatTTT aaaaaatgct attgtatata atagtatgta tgaaaattTT
3181 agtactagct tttggataag aattcctaag tattTTtaaca gtataagtct aaataatgaa
3241 tatacaataa taaattgtat ggaaaaataat tcaggatgga aagtatcact taattatggt
3301 gaaataatct ggactTTTaca ggatactcag gaaataaaaac aaagagtagt tTTTaaatac
3361 agtcaaatga ttaatatatc agattatata aacagatgga tTTTtgtaac tatcactaat
3421 aatagattaa ataactctaa aatttatata aatggaagat taatagatca aaaaccaatt
3481 tcaaatTTtag gtaatattca tgctagtaat aatataatgt tTaaattaga tggTtgtaga
3541 gatacacata gatatatTTg gataaaaatat tTTaatctTT ttgataagga attaaatgaa
3601 aaagaaatca aagattTata tgataatcaa tcaaattcag gtattTTTaaa agactTTTgg
3661 ggtgattatt tacaatatga taaaccatac tatatgtTaa atttatatga tccaaataaa
3721 tatgtcgatg taaataatgt aggtattaga ggTtatatgt atctTaaagg gcctagaggt
3781 agcgtaatga ctacaaacat ttattTaaat tcaagttTgt atagggggac aaaatttatt
3841 ataaaaaaat atgcttctgTg aaataaaagat aatattgtta gaaataatga tcgtgtatat
3901 attaatgtag tagtTaaaaa taaagaatat aggttagcta ctaatgcac acaggcaggc
3961 gtagaaaaaa tactaagtgc attagaaata cctgatgtag gaaatctaag tcaagtagta
4021 gtaatgaagt caaaaaatga tcaaggaata acaaaataaat gcaaaatgaa tttacaagat
4081 aataatggga atgatatagg cTTtatagga tttcatcagt tTaaataat agctaaacta
4141 gtagcaagta attggtataa tagacaaata gaaagatcta gtaggactTT gggTtgctca
4201 tgggaattta tTcctgtaga tgatggatgg ggagaaaggc cactgtaatt aatctcaaac
4261 tacatgagtc tgtcaagaat tTtctgTaaa catccataaa aattTTtaaa ttaatatgtt
4321 taagaataac tagatatgag tattgtTTga actgcccctg tcaagtagac aggtaaaaaa
4381 ataaaaatta agatactatg gtctgatttc gatattctat cggagtcaga cTTTTaact
4441 tttcttgtat cTTTTttgta ttgtaaaact ctatgtattc atcaattgca agttccaatt
4501 agtcaaaatt atgaaactTT ctaagataat acatttctga tTTTataatt tcccaaaatc
4561 cttccatagg accattatca atacatctac caactcgaga catactTTTga gttgcgccta
4621 tctcattaag tttattcttg aaagatttac ttgtatattg aaaaccgcta tcactgtgaa
4681 aaagtggact agcatcagga ttggaggtaa ctgctttatc aaaggTTTca aagacaagga
4741 cgTTgttatt tgattTTcca agtacatagg aaataatgct attatcatgc aaatcaagta
4801 tttcactcaa gtacgcctTT gTTtcgtctg tTaaac

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10

[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[OMIM](#)
[Books](#)

Search for

Range: from to ☐ Reverse complemented strand Features: ☐ SNP

☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: X52066. Reports *Clostridium botul...*[gi:40381]

[Links](#)

LOCUS CBBOTAG 4292 bp DNA linear BCT 12-SEP-1993
 DEFINITION *Clostridium botulinum* botA gene for type A neurotoxin.
 ACCESSION X52066 X52088
 VERSION X52066.1 GI:40381
 KEYWORDS botA gene; neurotoxin; secreted protein.
 SOURCE *Clostridium botulinum*
 ORGANISM *Clostridium botulinum*
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 Clostridium.
 REFERENCE 1 (bases 1 to 4292)
 AUTHORS Thompson,D.E., Brehm,J.K., Oultram,J.D., Swinfield,T.J.,
 Shone,C.C., Atkinson,T., Melling,J. and Minton,N.P.
 TITLE The complete amino acid sequence of the *Clostridium botulinum* type
 A neurotoxin, deduced by nucleotide sequence analysis of the
 encoding gene
 JOURNAL Eur. J. Biochem. 189 (1), 73-81 (1990)
 PUBMED 2185020
 REFERENCE 2 (bases 1 to 4292)
 AUTHORS Minton,N.P.
 TITLE Direct Submission
 JOURNAL Submitted (08-JAN-1990) Minton N.P., PHLS Centre for Applied
 Microbiology & Research, Molecular Genetics Group, Division of
 Biotechnology, Porton Down, Salisbury SP4 0JG Wiltshire, U K
 FEATURES Location/Qualifiers
 source 1..4292
 /organism="Clostridium botulinum"
 /mol_type="genomic DNA"
 /strain="sub sp. type A, NCTC2916"
 /db_xref="taxon:1491"
 misc_feature 16..64
 /note="dyad symmetry"
 promoter 19..24
 /note="-35 region"
 promoter 41..46
 /note="-10 region"
 RBS 63..68
 /note="ribosome binding site"
 CDS 77..3967
 /note="unnamed protein product; type A neurotoxin (AA
 1-1296)"
 /codon_start=1
 /transl_table=11
 /protein_id="CAA36289.1"
 /db_xref="GI:40382"

```

/db_xref="GOA:P10845"
/db_xref="UniProt/Swiss-Prot:P10845"
/translation="MQFVNKQFNYKDPVNGVDIAYIKIPNVGQMOPVKAFKIHNKIWW
IPERDTFTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYLKGVTCLFERIYSTD
LGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELNLVIGPSADI
IQFECKSFGEVLNLTRNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAAGKATDPA
VTLAHELHAGHRLYGIAPNPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDS
LQENEFRLYYNKFKDIASTLNKAKSIVGTASLQYMKNVFKEKYLLSEDTSGKFSVD
KLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDAVKINIVPKVNYTIYDGFNL
RNTNLAANFNGQNTNINNMNFTKLKNTGLFEFYKLLCVRGIITSKTKSLDKGYNKAL
NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSNTNIEAAEENISLDLIQQYYLTFNF
DNEPENISIEENLSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFHKGSR
ALTNSVNEALLNPSRVYTFSSDYVKKVKNKATEAAMFLGWVEQLVYDFTDETSEVSTT
DKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALV
SYIANKVLTQVIDNALSKRNEKWDEVYKIVTNWLAKVNTQIDLRKKMKEALENQ
EATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMN
SMIPYGVKRLDFDASLKDALLKYIYDNRGTLIGQVDRKDKVNNLTSTDIPIFQLSKY
VDNQRLSTFTYIKNIINTSILNRYESNHLIDLSRYASKINIGSKVNFDPIDKNQI
QLFNLESSKIEVILKNAIVYNSMYENFSTSWIRIPKYFNSISLNNEYTIINCMENNS
GWKVSILNYGEIITWLTQDTQEIQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIY
INGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIYFNLFDKELNEKEIKDLY
DNQSNNGILKDFWDYLDQYDKPYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTT
NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEK
ILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNAIKLV
ASNWYNRQIERSRSLTLCGSWEFIPVDDGWGERPL"

```

misc feature

4042..4087

/note="dyad symmetry"

misc feature

4104..4136

/note="dyad symmetry"

misc feature

4158..4188

/note="dyad symmetry"

ORIGIN

```

1 tcaaagtatt tgtatttatg gtcatttaaa taattaataa ttttaattaat tttaaatatt
61 ataagagggtg ttaaatatgc aatttggttaa taaacaattt aattataaag atcctgtaaa
121 tgggtgtgat attgcttata taaaaattcc aaatgtagga caaatgcaac cagtaaaagc
181 ttttaaaaatt cataataaaa tatgggttat tccagaaaga gatacattta caaatcctga
241 agaaggagat ttaaatccac caccagaagc aaaacaagtt ccagtttcat attatgattc
301 aacatatatta agtacagata atgaaaaaga taattattta aaggaggatg caaaattatt
361 tgagagaatt tattcaactg atcttggaag aatgttggtt acatcaatag taaggggaat
421 accatthttg ggtggaagta caatagatac agaattaaaa gttattgata ctaattgtat
481 taatgtgata caaccagatg gtagttatag atcagaagaa cttaatctag taataatagg
541 accctcagct gatattatac agtttgaatg taaaagcttt ggacatgaag ttttgaatct
601 tacgcgaaat ggttatggct ctactcaata cattagattt agcccagatt ttacatttgg
661 ttttgaggag tcacttgaag ttgatacaaa tcctctttta ggtgcaggca aatttgctac
721 agatccagca gtaacattag cacatgaact tatacatgct ggacatagat tatatggaat
781 agcaattaat ccaaataggg tttttaaagt aaataactaat gcctattatg aaatgagtg
841 gttagaagta agctttgagg aacttagaag atttggggga catgatgcaa agtttataga
901 tagttttacag gaaaacgaat ttcgtctata ttattataat aagtttaaag atatagcaag
961 tacacttaat aaagctaaat caatagtagg tactactgct tcattacagt atatgaaaaa
1021 tgttttttaa gagaaatata tcctatctga agatacatct ggaaaatttt cggtagataa
1081 attaaaattt gataagttat acaaaatggt aacagagatt tacacagagg ataattttgt
1141 taagtthttt aaagtactta acagaaaaac atatttgaat tttgataaag ccgtatttaa
1201 gataaatata gtacctaaag taaattacac aatatatgat ggatttaatt taagaaatac
1261 aaatttagca gcaaacctta atggtcaaaa tacagaaatt aataatatga attttactaa
1321 actaaaaaat tttactggat tgtttgaatt ttataagttg ctatgtgtaa gagggataat
1381 aacttctaaa actaaatcat tagataaagg atacaataag gcattaaatg atttatgtat
1441 caaagttaat aattgggact tgttttttag tccttcagaa gataatttta ctaatgatct
1501 aaataaagga gaagaaatta catctgatac taatatagaa gcagcagaag aaaatattag
1561 ttttagattta atacaacaat attatttaac ctttaatttt gataatgaac ctgaaaatat
1621 ttcaatagaa aatctttcaa gtgacattat aggccaatta gaacttatgc ctaatataga

```


1681 aagatttcct aatggaaaaa agtatgagtt agataaatat actatgttcc attatcttcg
1741 tgctcaagaa tttgaacatg gtaaatctag gattgcttta acaaattctg ttaacgaagc
1801 attattaaat cctagtcgtg tttatacatt tttttcttca gactatgtaa agaaagttaa
1861 taaagctacg gaggcagcta tgttttttagg ctgggtagaa caattagtat atgattttac
1921 cgatgaaact agcgaagtaa gtactacgga taaaattgcg gatataacta taattattcc
1981 atatatagga cctgctttaa atatatgtaa tatgtttatat aaagatgatt ttgtagggtgc
2041 ttttaattttt tcaggagctg ttattctgtt agaatttata ccagagattg caataacctgt
2101 attagggtact tttgcacttg tatcatatat tgcgaataag gttctaaccg ttcaaacaat
2161 agataatgct ttaagtaaaa gaaatgaaaa atgggatgag gtctataaat atatagtaac
2221 aaattgggtta gcaaagggtta atacacagat tgatctaata agaaaaaaaaa tgaagaagc
2281 tttagaaaaat caagcagaag caacaaaggc tataataaac tatcagtata atcaatatac
2341 tgaggaagag aaaaaataata ttaatttttaa tattgatgat ttaagttcga aacttaatga
2401 gtctataaat aaagctatga ttaatataaa taaatttttg aatcaatgct ctgtttcata
2461 tttaatgaat tctatgatcc cttatgggtgt taaacgggtta gaagattttg atgctagtct
2521 taaagatgca ttattaaagt atatatatga taatagagga actttaattg gtcaagtaga
2581 tagattaaaa gataaagtta ataatacact tagtacagat ataccttttc agctttccaa
2641 atacgtagat aatcaaagat tattatctac atttactgaa tatattaaga atattattaa
2701 tacttctata ttgaatttaa gatatgaaag taatcattta atagacttat ctaggtatgc
2761 atcaaaaaata aatattggta gtaaaagttaa ttttgatcca atagataaaa atcaaattca
2821 attatttaaat ttagaaaagta gtaaaattga ggtaatttta aaaaatgcta ttgtatataa
2881 tagtatgtat gaaaatttta gtactagctt ttggataaga attcctaagt attttaacag
2941 tataagtcta aataatgaat atacaataat aaattgtatg gaaaataatt caggatggaa
3001 agtatcactt aattatggtg aaataatctg gactttacag gatactcagg aaataaaaca
3061 aagagtagtt tttaaataca gtcaaagat taatatatca gattatataa acagatggat
3121 ttttgtaact atcactaata atagattaaa taactctaaa atttatataa atggaagatt
3181 aatagatcaa aaaccaattt caaatttagg taatattcat gctagtaata atataatggt
3241 taaattagat ggttgtagag atacacatag atatatgtg ataaaaatatt ttaatctttt
3301 tgataaggaa ttaaattgaaa aagaaatcaa agatttatat gataatcaat caaattcagg
3361 tatttttaaaa gacttttggg gtgattattt acaatatgat aaaccatact atatgttaaa
3421 tttatatgat ccaaataaat atgtcgaagt aaataatgta ggtattagag gttatatgta
3481 tcttaaaggg cctagaggta gcgtaatgac tacaaacatt tatttaaaatt caagtttgta
3541 taggggggaca aaatttatta taaaaaaata tgcttctgga aataaagata atattgttag
3601 aaataatgat cgtgtatata ttaatgtagt agttaaaaat aaagaatata ggtagctac
3661 taatgcatca caggcaggcg tagaaaaaat actaagtgca ttagaaatac ctgatgtagg
3721 aaatctaagt caagtagtag taatgaagtc aaaaaatgat caaggaataa caaataaatg
3781 caaaatgaat ttacaagata ataattggaa tgatataggc tttataggat ttcacagtt
3841 taataatata gctaaactag tagcaagtaa ttggtataat agacaaatag aaagatctag
3901 taggactttg ggttgctcat gggaatttat tcctgtagat gatggatggg gagaaaggcc
3961 actgtaatta atctcaaaact acatgagtct gtcaagaatt ttctgtaaac atccataaaa
4021 atttttaaat taatatgttt aagaataact agatatgagt attgctatgc taatatctag
4081 ttatttttaatt ttattcaata ttattacagt aagaaaaaat actattttta ttgtaaatac
4141 aagtttagtg gtatatctca taaatgatac aagatatcat tataatgatt ttgcaaatta
4201 tagttttgaa taaatatatt tacagtattt ttgaaatgat aataattact tcaaattctt
4261 tagtataatt ttttaatgtc ttaattttta ca

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

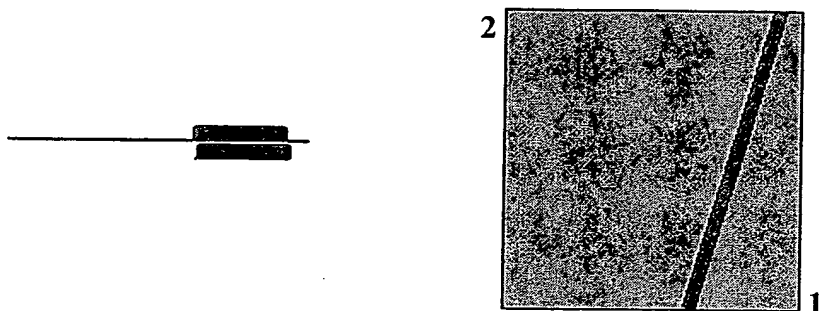
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:

x_dropoff: expect: wordsize: Filter ☒ Align ☐

Sequence 1 [gi_40381](#) Clostridium botulinum botA gene for type A neurotoxin **Length** 4292 (1 .. 4292)

Sequence 2 lcl|seq 2

Length 1323 (1 .. 1323)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 412 bits (214), Expect = e-111

Identities = 937/1302 (71%)

Strand = Plus / Plus

Query: 2666 tctacatttactgaatatattaagaatattattaatacttctatattgaatttaagatat 2725

Sbjct: 16 tctaccttcactgaatacatcaagaacatcatcaatacctccatcctgaacctgcgctac 75

Query: 2726 gaaagtaatcatttaatagacttatctaggtatgcatcaaaaataaatattggtagtaaa 2785

[illegible]

Query: 2786 gtaaatTTTgatccaatagataaaaaatcaaattcaattattttaatttagaaagtagtaaa 2845

Sbjct: 136 gttaacttcgatccgatcgacaagaatcagatccagctgttcaatctggaattcttccaaa 195



Query: 2846 attgaggtaat~~ttt~~aaaaaatgctattgtatataatagtatgtatgaaaattttagtact 2905

Sbjct: 196 atcgaagttatcctgaagaatgctatcgatacaactctatgtacgaaaacttctccacc 255

h cb hg b b e b cg

h cb h g b b e b cg

X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)



 My NCBI [\[Sign In\]](#) [\[Register\]](#)

[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [OMIM](#) [Books](#)

Search for

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Display Show

Range: from to Features:

1: [P04958](#). Reports Tetanus toxin pre...[gi:135624]

[BLink](#), [Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS P04958 1315 aa linear BCT 18-APR-2006
 DEFINITION Tetanus toxin precursor (Tentoxylisin) [Contains: Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy chain (Tetanus toxin chain H)].
 ACCESSION P04958
 VERSION P04958 GI:135624
 DBSOURCE swissprot: locus TETX_CLOTE, accession [P04958](#); class: standard. plasmid:pE88,7,created: Aug 13, 1987. sequence updated: Aug 13, 1987. annotation updated: Apr 18, 2006.
 xrefs: [X04436.1](#), [CAA28033.1](#), [X06214.1](#), [CAA29564.1](#), [AF528097.1](#), [AAO37454.1](#), [M12739.1](#), [AAA23282.1](#), [BTCLTN](#), [1A8D_](#), [1AF9_](#), [1DQHA](#), [1DFQA](#), [1DIWA](#), [1DLA](#), [1FV2A](#), [1FV3A](#), [1FV3B](#), [1YVGA](#), [1YXWA](#), [1YYNA](#), [1Z7HA](#)
 xrefs (non-sequence databases): MEROPS:M27.001, GenomeReviews:AF528097_GR, LinkHub:P04958, InterPro:IPR011591, InterPro:IPR008985, InterPro:IPR013320, InterPro:IPR011065, InterPro:IPR006025, InterPro:IPR000395, InterPro:IPR013104, InterPro:IPR012928, InterPro:IPR012500, Pfam:PF01742, Pfam:PF07951, Pfam:PF07953, Pfam:PF07952, PRINTS:PR00760, ProDom:PD001963, PROSITE:PS00142
 KEYWORDS 3D-structure; Complete proteome; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Plasmid; Protease; Toxin; Zinc.
 SOURCE *Clostridium tetani*
 ORGANISM *Clostridium tetani*
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
 REFERENCE 1 (residues 1 to 1315)
 AUTHORS Eisel,U., Jarausch,W., Goretzki,K., Henschen,A., Engels,J., Weller,U., Hudel,M., Habermann,E. and Niemann,H.
 TITLE Tetanus toxin: primary structure, expression in *E. coli*, and homology with botulinum toxins
 JOURNAL EMBO J. 5 (10), 2495-2502 (1986)
 PUBMED 3536478
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 PLASMID=75 Kbp
 REFERENCE 2 (residues 1 to 1315)
 AUTHORS Fairweather,N.F. and Lyness,V.A.
 TITLE The complete nucleotide sequence of tetanus toxin
 JOURNAL Nucleic Acids Res. 14 (19), 7809-7812 (1986)
 PUBMED 3774547

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=CN3911; PLASMID=75 Kbp

REFERENCE 3 (residues 1 to 1315)
AUTHORS Brueggemann,H., Baeumer,S., Fricke,W.F., Wiezer,A., Liesegang,H., Decker,I., Herzberg,C., Martinez-Arias,R., Merkl,R., Henne,A. and Gottschalk,G.
TITLE The genome sequence of Clostridium tetani, the causative agent of tetanus disease
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1316-1321 (2003)
PUBMED [12552129](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=Massachusetts / E88; PLASMID=pE88

REFERENCE 4 (residues 1 to 1315)
AUTHORS Fairweather,N.F., Lyness,V.A., Pickard,D.J., Allen,G. and Thomson,R.O.
TITLE Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in Escherichia coli
JOURNAL J. Bacteriol. 165 (1), 21-27 (1986)
PUBMED [3510187](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 742-1314.
PLASMID=75 Kbp

REFERENCE 5 (residues 1 to 1315)
AUTHORS Krieglstein,K., Henschen,A., Weller,U. and Habermann,E.
TITLE Arrangement of disulfide bridges and positions of sulfhydryl groups in tetanus toxin
JOURNAL Eur. J. Biochem. 188 (1), 39-45 (1990)
PUBMED [2108021](#)

REMARK PARTIAL PROTEIN SEQUENCE, AND DISULFIDE BONDS.

REFERENCE 6 (residues 1 to 1315)
AUTHORS Krieglstein,K.G., Henschen,A.H., Weller,U. and Habermann,E.
TITLE Limited proteolysis of tetanus toxin. Relation to activity and identification of cleavage sites
JOURNAL Eur. J. Biochem. 202 (1), 41-51 (1991)
PUBMED [1935979](#)

REMARK PARTIAL PROTEIN SEQUENCE.

REFERENCE 7 (residues 1 to 1315)
AUTHORS Schiavo,G., Poulain,B., Rossetto,O., Benfenati,F., Tauc,L. and Montecucco,C.
TITLE Tetanus toxin is a zinc protein and its inhibition of neurotransmitter release and protease activity depend on zinc
JOURNAL EMBO J. 11 (10), 3577-3583 (1992)
PUBMED [1396558](#)

REMARK IDENTIFICATION AS ZINC-PROTEASE.

REFERENCE 8 (residues 1 to 1315)
AUTHORS Schiavo,G., Benfenati,F., Poulain,B., Rossetto,O., Polverino de Laureto,P., DasGupta,B.R. and Montecucco,C.
TITLE Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin
JOURNAL Nature 359 (6398), 832-835 (1992)
PUBMED [1331807](#)

REMARK IDENTIFICATION OF SUBSTRATE.

REFERENCE 9 (residues 1 to 1315)
AUTHORS Umland,T.C., Wingert,L.M., Swaminathan,S., Furey,W.F., Schmidt,J.J. and Sax,M.
TITLE Structure of the receptor binding fragment HC of tetanus neurotoxin
JOURNAL Nat. Struct. Biol. 4 (10), 788-792 (1997)
PUBMED [9334741](#)

REMARK X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.

COMMENT On Apr 12, 2005 this sequence version replaced [gi:69647](#).
[FUNCTION] Tetanus toxin acts by inhibiting neurotransmitter

release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 76-Gln-|-Phe-77 bond of synaptobrevin-2.

[CATALYTIC ACTIVITY] Hydrolysis of 76-Gln-|-Phe-77 bond in synaptobrevin 2.

[COFACTOR] Binds 1 zinc ion per subunit (By similarity).

[SUBUNIT] The precursor polypeptide is subsequently cleaved to yield subchains L and H. These remain linked by a disulfide bridge and are non-toxic after separation.

[MISCELLANEOUS] The C-terminus of the heavy chain binds to ganglioside receptors.

[SIMILARITY] Belongs to the peptidase M27 family.

FEATURES	Location/Qualifiers
<u>source</u>	1..1315 /organism="Clostridium tetani" /plasmid="" /db_xref="taxon:1513"
<u>gene</u>	1..1315 /gene="tetX" /locus_tag="CTC_p60"
<u>Protein</u>	1..1315 /gene="tetX" /locus_tag="CTC_p60" /product="Tetanus toxin precursor" /EC_number="3.4.24.68"
<u>Region</u>	2..457 /gene="tetX" /locus_tag="CTC_p60" /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="Tetanus toxin light chain. /FTId=PRO_0000029229."
<u>Site</u>	233 /gene="tetX" /locus_tag="CTC_p60" /site_type="metal-binding" /inference="non-experimental evidence, no additional details recorded" /note="Zinc (catalytic) (By similarity)."
<u>Site</u>	234 /gene="tetX" /locus_tag="CTC_p60" /site_type="active" /inference="non-experimental evidence, no additional details recorded" /note="By similarity."
<u>Site</u>	237 /gene="tetX" /locus_tag="CTC_p60" /site_type="metal-binding" /inference="non-experimental evidence, no additional details recorded" /note="Zinc (catalytic) (By similarity)."
<u>Bond</u>	bond(439,467) /gene="tetX" /locus_tag="CTC_p60" /bond_type="disulfide"

Region /experiment="experimental evidence, no additional details recorded"
/note="Interchain (between light and heavy chains)."
458..1315
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Mature chain"
/experiment="experimental evidence, no additional details recorded"
/note="Tetanus toxin heavy chain. /FTId=PRO_0000029230."
Region 868
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 872
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 875
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 877..883
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
Region 884
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
Region 885..892
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 893..894
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
Region 895..898
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
Region 900..902
/gene="tetX"

Region /locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
905..908
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 910..911
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 913..916
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 918..928
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 929..930
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 933..936
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 939..941
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

Region 942..947
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 948
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 950..957
/gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"
963..969
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 970..971
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 973..978
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 981..982
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 984..986
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 988..996
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 997..998
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 999..1005
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1007..1008
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1009
 /gene="tetX"

Region /locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
1011..1017
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 1020..1021
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 1022..1023
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 1024
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 1026..1030
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 1032..1038
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 1040..1041
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 1042..1048
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

Region 1049..1050
/gene="tetX"
/locus_tag="CTC_p60"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region 1051..1057
/gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"
1059..1060
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1068..1076
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Bond bond(1077,1093)
 /gene="tetX"
 /locus_tag="CTC_p60"
 /bond_type="disulfide"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1080..1081
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1083..1094
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1098..1106
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1107..1108
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1111..1113
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1115
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1117..1118
 /gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"
1119..1121
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1123
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1124..1125
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1128..1132
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1133..1135
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1136..1137
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1138..1144
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1145..1146
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1147
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1149..1153
 /gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"
1156..1159
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1160..1163
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1164..1167
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1170
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1172
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1174..1181
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1185..1186
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1189
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1191
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1192..1193
 /gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"
1194..1202
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1203..1204
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1205..1212
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1213..1214
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1217..1218
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1219..1221
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1222..1224
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1226..1228
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1232..1233
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1236..1237
 /gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"
1239..1243
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1246
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1248..1249
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1250
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1253..1258
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1260..1262
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1264..1273
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1275
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1276..1277
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1278
 /gene="tetX"

Region /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"
1281..1287
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1288..1293
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1294..1295
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1296..1298
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1300..1301
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1303..1306
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1309
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1310..1311
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Hydrogen bonded turn"
 /experiment="experimental evidence, no additional details
 recorded"

Region 1312
 /gene="tetX"
 /locus_tag="CTC_p60"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details
 recorded"

ORIGIN

1 mpitinnfry sdpvnndtii mmeppyckgl diyykafkit driwivpery efgtkpedfn

61 ppssliegas eyydpnylrt dsdkdrflqt mvklfnrikn nvagealldk iinaipylgn
121 syslldkfdt nsnsvsfnll eqdpsgattk samltlnliif gpgpvlknkne vrgivlrvdn
181 knyfpcrdggf gsimqmafcp eyvptfdnvi enitsltigk skyfqdpall lmhelihvlh
241 glygmqvssh eiipskqei ymhtypisae elftfggqda nlisidiknd lyektlndyk
301 aianklsqvt scndpnidid sykqiyqqky qfdkdsngqy ivnedkfqil ynsimygfte
361 ielgkknfnik trlsyfsnmh dpvkipnll dtyndtegf nieskdlkse ykggmrvnt
421 nafrnvdgsg lvskliglck kiipptnire nlynrtaslt dlggelciki knedltfaie
481 knsfseepfq deivsyntkn kplnfnysld kiivdynlqs kitlpndrtt pvtkgipyap
541 eyksnaasti eihnidnti yqylyaqksp ttlgritmtn svddalinst kiysyfpsvi
601 skvnqgaqgi lflqwvrddi ddftnessqk ttidkisdvs tivpyigpal nivkqgyegn
661 figalettg vllleyipei tlpviaalsi aesstqkeki iktidnflek ryekwievyk
721 lvkakwlgvt ntqfqkrsyq myrsleyqvd aikkiidyey kiysgpdkeq iadeinnlkn
781 kleeekankam ininifmres srsflvnqmi neakkqllef dtqsknilmq yikanskfig
841 itelkklesk inkvfstpip fsysknldcw vdneedidvi lkkstilnld inndiisdis
901 gfnssvityp daqlvpging kaihlvnes sevivhkamd ieyndmfnnf tvsfwlrvpk
961 vsashleqyg tneysiissm kkhsisigsg wsvslkgnnl iwtlkdsage vrqitfrdlp
1021 dkfnaylank wvfititndr lssanlying vlmgsaeitg lgairednni tlkldrcnnn
1081 ngyvsidkfr ifckalnpke ieklytsyls itflrdfwgn plrydteyy1 ipvassskdv
1141 qlknitdymy ltnapsytng kluiyyrrly nglkfiikry tpnneidsfv ksgdfiklyv
1201 synnnehivg ypkdgnafnn ldrilrvgyn apgiplaykkm eavklrdlkt ysvqlklydd
1261 knaslglvgt hngqigndpn rdiliasnwy fnhlkdakilg cdwyfvptde gwtnd

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Apr 11 2006 19:57:30

 [ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Swiss-Prot](#) [Proteomics tools](#)

Search for

Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: SEQ (434 residues)
Sequence 2: TETX_CLOTE (1314 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

33.9% identity in 434 residues overlap; Score: 496.0; Gap frequency:

```

SEQ          14  TSILNLRYESNHLIDLTRYASKINIGSKVNFDP-IDKNQIQLFNLESSKIE
TETX_CLOTE   883  STILNLDINNDIISDISGFNSSVITYPDACLVPGLNGKAIHLVNNESSEVI
                ****          * * *          * *      * * * * *

SEQ          73  NSMYENFSTSFWIRIPKYFNSISLN--NEytiINCMENNS-----GWKVS
TETX_CLOTE   943  NDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVS
                * *  **   *** * **   *          *** **  *   *      ** **

SEQ         125  LQDTQEIKQRVVFKEYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLID
TETX_CLOTE  1003  LKDSAGEVRQITFRDLDPKFNAYLANKWVFITITNDRLSSANLYINGVLMG
                * *          *          * * * * * * *      * * * *

SEQ         185  IHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILI
TETX_CLOTE  1063  IREDNNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLI
  
```

```

          *   ***   ***   *           *   *   *   *   *   *   *   *   *
SEQ          245 YDKPYMYMLNLYDPNKYVDVNNVGIRGYMYL-KGPRGSVMTTNIYLNSSLYR(
TETX_CLOTE  1123 YDTEYYLIPVASSSKDVQLKN--ITDYMylTNAPSYTNGKLNIIYRR-LYN(
          **   **           *   *   *   *   *   *   *   *   *   *

```

```

SEQ          304 ASGNK-DNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIP-DV(
TETX_CLOTE  1180 TPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNFNNLDRILRVGYNAI
          *   *   *   *           *   *   *

```

```

SEQ          362 KSKNDQGI-TNKCKMNLQDNNGNDIGFIGFH--QFNNTIAK--LVASNWYNI
TETX_CLOTE  1240 EAVKLRLDKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFI
          *           *   *           *   *   *   *   *   *   *

```

```

SEQ          416 LGCSWEFIPVDDGW
TETX_CLOTE  1298 LGCDWYFVPTDEGW
          *** * * * * *

```

39.1% identity in 23 residues overlap; Score: 39.0; Gap frequency: 0

```

SEQ          141 QMINISDYINRWIFVTITNNRLN
TETX_CLOTE  1140 QLKNITDYMylTNAPSYTNGKLN
          *   **   **           **   **

```

31.4% identity in 35 residues overlap; Score: 35.0; Gap frequency: 0

```

SEQ          81 TSFWIRIPKYFNSISLNNNEYTIINCMENNSGWKVS
TETX_CLOTE  213 TSLTIGKSKYFQDPALLMHელიHVLHGLYGMQVS
          **   *   ***   *           *           *   **

```

32.6% identity in 46 residues overlap; Score: 33.0; Gap frequency: 2

```

SEQ          3 TFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPID
TETX_CLOTE  273 TFGGQDANLISIDIKNDLYEKT-LNDYKAIANKLSQVTSCNDPNID
          **           *   *   *   *   **   *   *   *   *   *

```

31.2% identity in 16 residues overlap; Score: 32.0; Gap frequency: 0

```

SEQ          155 VTITNNRLNNSKIYIN
TETX_CLOTE  1069 ITLKLDRCNNNNQYVS
          *           *   **   *

```

33.3% identity in 15 residues overlap; Score: 32.0; Gap frequency: 0

SEQ 96 LNNEYTIINCMENNS
TETX_CLOTE 117 LGNSYSLLDKFDTNS
* * * **

50.0% identity in 12 residues overlap; Score: 32.0; Gap frequency: 0

SEQ 162 LNNSKIYINGRL
TETX_CLOTE 1150 LTNAPSYTNGKL
* * * * *

36.8% identity in 19 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 3 TFTEYIKNIINTSILNLRY
TETX_CLOTE 204 TFDNVIENTISLTIGSKY
** * ** * *

27.8% identity in 18 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 245 YDKPYMMLNLYDPNKYVD
TETX_CLOTE 1169 YNGLKFIIKRYTPNNEID
* * ** *

50.0% identity in 12 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 62 IEVILKNAIVYN
TETX_CLOTE 876 IDVILKKSTILN
* **** *

40.0% identity in 15 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 218 NEKEIKDLYDNQSNS
TETX_CLOTE 119 NSYSLLDKFDTNSNS
* * * ***

29.3% identity in 41 residues overlap; Score: 30.0; Gap frequency: 2

SEQ 35 KINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSM
TETX_CLOTE 542 KSNAASTIEIHNIDDNTIYQY-LYAQKSPTTLQRITMTNSV
* * * ** * * * **

21.7% identity in 23 residues overlap; Score: 30.0; Gap frequency: 0

SEQ 35 KINIGSKVNFDPIDKNQIQLFNL
TETX_CLOTE 365 KFNKTRLSYFSMNHDPVKIPNL
* ** **

28.6% identity in 28 residues overlap; Score: 30.0; Gap frequency: 0

SEQ 316 DRVYINVVVKNKEYRLATNASQAGVEKI
TETX_CLOTE 278 DANLISIDIKNDLYEKTLDYKAIANKL
* * ** * * *

28.0% identity in 25 residues overlap; Score: 30.0; Gap frequency: 0

SEQ 142 MINISDYINRWIFVTITNNRLNNSK
TETX_CLOTE 789 MININIFMRESSRSFLVNQMINEAK
**** * * *

25.0% identity in 40 residues overlap; Score: 29.0; Gap frequency: 0

SEQ 211 NLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYY
TETX_CLOTE 617 DIIDDFTNES SQTTIDKISDVSTIVPYIGPALNIVKQGY
* ** * * * * *

22.8% identity in 79 residues overlap; Score: 29.0; Gap frequency: 3

SEQ 330 RLATNASQAGVEKILSALEIPDVG NLS-QVVMKSKNDQ-GITNKCKMNLQI
TETX_CLOTE 1225 RVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGI
* ** * * * * ** *

SEQ 388 IGFHQFN NIA-KLVASNWY
TETX_CLOTE 1285 ASNWYFNHLKDKILGCDWY
** * **

35.0% identity in 20 residues overlap; Score: 29.0; Gap frequency: 0

SEQ 362 KSKNDQGITNKCKMNLQDNN
TETX_CLOTE 333 KDSNGQYIVNEDKFQILYNS
* * * * * *

42.9% identity in 14 residues overlap; Score: 28.0; Gap frequency: 0

SEQ 67 KNAIVYNSMYENFS
TETX_CLOTE 345 KFQILYNSIMYGFT
* * *** *

20.7% identity in 58 residues overlap; Score: 28.0; Gap frequency: 0

SEQ 307 NKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ'
TETX_CLOTE 779 NKLEEKANKAMININIFMRESSRSFLVNQMINEAKKQLLEFDTQSKNILMQ'
* * * * * * * *

 [ExPASy Home page](#) [Site Map](#) [Search ExPASy](#) [Contact us](#) [Swiss-Prot](#) [Proteomics tools](#)